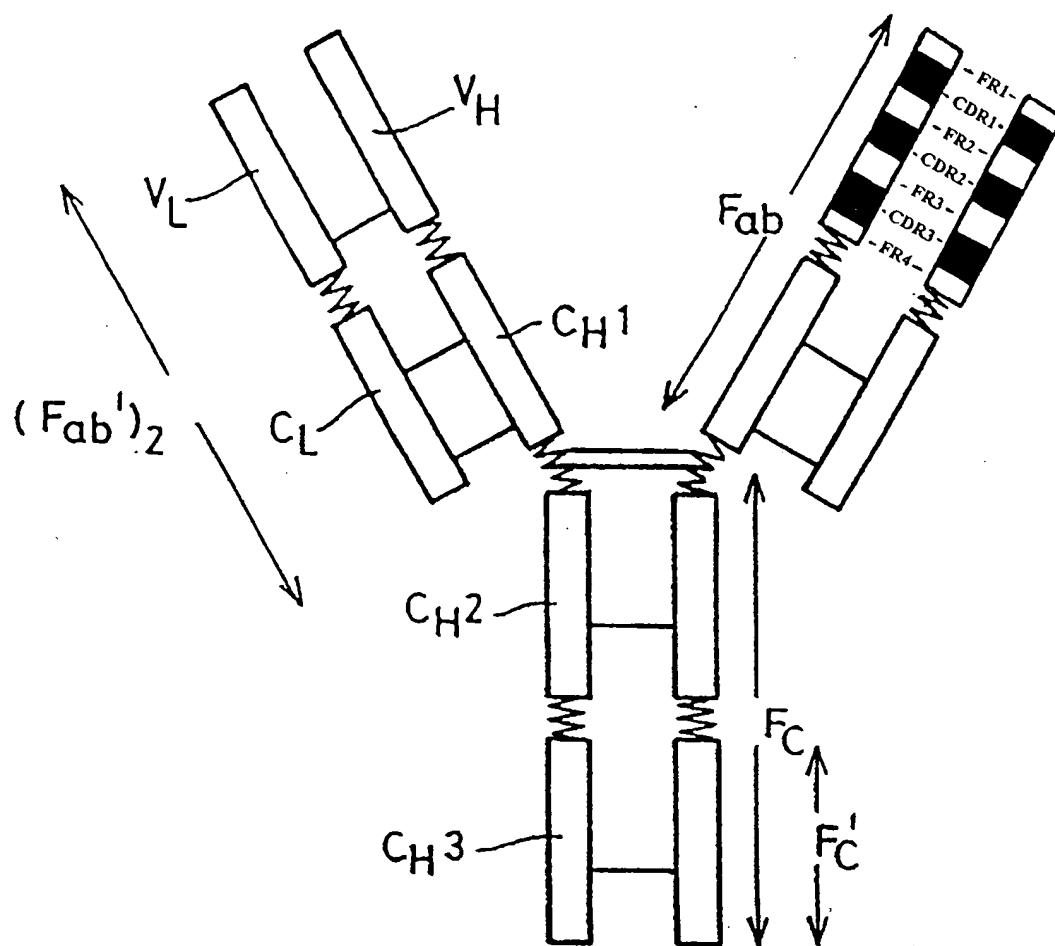


FIGURE 1



domains



inter-domain sections



disulphide bonds

V

variable

C

constant

L

light chain

H

heavy chain

## FIGURE 2

**A.**

**SEQ ID NO:59 - AME 33 light chain variable region amino acid sequence**

EIVLTQSPGTL<sup>SL</sup>SPGERATL<sup>SCR</sup>ASSVPYIHWYQQKPGQAPRLLIYAT<sup>S</sup>ALASGI  
PDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLEIK

**B.**

**SEQ ID NO:60 - AME 33 light chain variable region nucleic acid sequence**

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG  
AGCCACCCTCTCCTGCAGGGCCAGCTCAAGTGTACCGTACATCCACTGGTAC  
CAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCCACATCCGCTCT  
GGCTTCTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTC  
ACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCA  
GCAGTGGCTGAGTAACCCACCCACTTTTGGCCAGGGGACCAAGCTGGAGATC  
AAA

### FIGURE 3

**A.**

**SEQ ID NO:61 - AME 33 heavy chain variable region amino acid sequence**

EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYP  
LTGDTSYNQKSKLQVTISADKSISTAYLQWSSLKASDTAMYYCARSTYVGGDW  
QFDVWGKGTTVTVSS

**B.**

**SEQ ID NO:62 - AME 33 heavy chain variable region nucleic acid sequence**

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTTCTGGCCGTACATTTACCAGTTACAATATGCA  
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGGCTATTTAT  
CCCTTGACGGGTGATACTTCCTACAATCAGAAGTCGAAACTCCAGGTCACCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGATCGACTTACGTGGGCGGT  
GACTGGCAGTTCGATGTCTGGGGCAAGGGGACCACGGTCACCGTCTCCTCA

## FIGURE 4

**A. Amino acid sequence of a human light chain framework region VkIII (A27)  
(DPK22) with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:71)      CDRL1      (FRL2 - SEQ ID NO:72)      CDRL2  
EIVLTQSPGTLSPGERATLSCXXXXXXXXXXXX WYQQKPGQAPRLLIYXXXXXXXX  
(FRL3 - SEQ ID NO:73)      CDRL3      (FRL4 - SEQ ID NO:74)  
GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCXXXXXXXXXX FGQGTKLEIK

**B. Nucleic acid sequence of a human light chain framework region VkIII (A27)  
(DPK22) with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:75)  
GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAG  
CDRL1  
CCACCCTCTCCTGCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGGTACCAG  
(FRL2 - SEQ ID NO:76)      CDRL2  
CAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATXXXXXXXXXXXXXXXXXXXX  
XXXGGCATCCCAGACAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTC  
(FRL3 - SEQ ID NO:77)  
ACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTXXXXXXXXXX  
CDRL3      (FRL4 - SEQ ID NO:78)  
XXXXXXXXXXXXXXXXXXXXTTTGGCCAGGGGACCAAGCTGGAGATCAAA

## FIGURE 5

**A. Amino acid sequence of a human heavy chain framework region VH5-51  
(DP-73) with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:79) CDRH1 (FRH2 - SEQ ID NO:80)  
EVQLVQSGAEVKKPGESLKISCKGSXXXXXXXXXXXXWVRQMPGKGLEWMG

CDRH2 (FRH3 - SEQ ID NO:81)  
XXXXXXXXXXXXXXXXXXXXQVTISADKSISTAYLQWSSLKASDTAMYYCAR

CDRH3 (FRH4 - SEQ ID NO:82)  
XXXXXXXXXXXXWGKGTTTVTVSS

**B. Nucleic acid sequence of a human heavy chain framework region VH5-51  
(DP-73) with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:83)  
GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTG

CDRH1  
AAGATCTCCTGTAAGGGTCTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

(FRH2- SEQ ID NO:84)  
TGGGTGCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGG

CDRH2  
XX  
CAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGC

(FRH3 - SEQ ID NO:85)  
AGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGXXXXXXXXXXXX

CDRH3 (FRH4 - SEQ ID NO:86)  
XXXXXXXXXXXXXXXXXXXXTGGGGCAAGGGGACCACGGTCACCGTCT  
CCTCA

## FIGURE 6

A.

**SEQ ID NO:63 - AME 5 light chain variable region amino acid sequence**

DIQMTQSPSSLSASVGDRVTITCRASSSVHYIHWYQQKPGKVPKLLIYATSGLAS  
GVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQTWTFNPPTFGGGTKVEIK

B.

**SEQ ID NO:64 - AME 5 light chain variable region nucleic acid sequence**

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGA  
GACAGAGTCACCATCACTTGCAGGGCCAGCTCAAGTGTACATTACATC  
CACTGGTACCAGCAGAAACCAGGGAAAGTTCCTAAGCTCTTGATCTAT  
GCCACATCCGGCCTGGCTTCTGGGGTCCCATCTCGGTTCAGTGGCAGT  
GGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAA  
GATGTTGCCACTTATTACTGCCAGACTTGGACTTTTAACCCTCCCACG  
TTCGGCGGAGGGACCAAGGTGGAGATCAAA

## FIGURE 7

**A.**

**SEQ ID NO:65 - AME 5 heavy chain variable region amino acid sequence**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNMHWVRQAPGQGLEWMGAIY  
PGNGDTSYNQKFKWRVTMTRDTSTSTVYMELSSLRSEDVAVYYCARSTYYGGD  
WQFDEWGKGTTVTVSS

**B.**

**SEQ ID NO:66 - AME 5 heavy chain variable region nucleic acid sequence**

CAGGTGCAGCTGGTGCAGTCTGGTGCTGAAGTGAAGAAGCCTGGGGCC  
TCAGTGAAGGTGTCCTGCAAGGCATCTGGATACACCTTCACCAGCTAC  
AATATGCACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATG  
GGAGCCATCTATCCTGGAAATGGTGATACAAGCTACAATCAGAAGTTT  
AAATGGAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTAC  
ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT  
GCGAGATCGACTTATTACGGCGGTGACTGGCAGTTCGACGAGTGGGGC  
AAAGGGACCACGGTCACCGTCTCCTCA

### FIGURE 8

**A. Amino acid sequence of a human light chain framework region VkI (DPK4) (A20) with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:87) (CDRL1) (FRL2 - SEQ ID NO:88) (CDRL2)  
DIQMTQSPSSLSASVGDRVTITCXXXXXXXXXXWYQQKPGKVPKLLIYXXXXXXXX  
(FRL3 - SEQ ID NO:89) (CDRL3) (FRL4 - SEQ ID NO:90)  
GVPSRFSGSGSGTDFLTITSLQPEDVATYYCXXXXXXXXXXFGGGTKVEIK

**B. Nucleic acid sequence of a human light chain framework region VkI (DPK4) (A20) with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:91)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAG

(CDRL1)

TCACCATCACTTGCXXXXXXXXXXXXXXXXXXXXXXXXXXTGGTACCAG

(FRL2 - SEQ ID NO:92)

(CDRL2)

CAGAAACCAGGGAAAGTTCCTAAGCTCTTGATCTATXXXXXXXXXXXXXXXXXX

(CDRL2 cont.)

(FRL3 - SEQ ID NO:93)

XXXXGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCT

CACCATCAGCAGCCTGCAGCCTGAAGATGTTGCCACTTATTACTGCXXXXXXXXX

(CDRL3)

(FRL4 - SEQ ID NO:94)

XXXXXXXXXXXXXXXXXXXXTTCGGCGGAGGGACCAAGGTGGAGA

TCAA



## FIGURE 9

**A. Amino acid sequence of a human heavy chain framework region VHI DP7/21-2 with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:95) (CDRH1) (FRH2 - SEQ ID NO:96)  
QVQLVQSGAEVKKPGASVKVSCKASXXXXXXXXXXWVRQAPGQGLEWMG  
(CDRH2) (FRH3 - SEQ ID NO:97)  
XXXXXXXXXXXXXXXXXXRVMTTRDTSTSTVYMESSLRSEDVAVYYCAR  
(CDRH3) (FRH4 - SEQ ID NO:98)  
XXXXXXXXXXXXXXXXXWGKGTITVTVSS

**B. Nucleic acid sequence of a human heavy chain framework region VHI DP7/21-2 with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:99)  
CAGGTGCAGCTGGTGCAGTCTGGTGCTGAAGTGAAGAAGCCTGGGGCCTCAGTG  
(CDRH1)  
AAGGTGTCCTGCAAGGCATCTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTG  
(FRH2 - SEQ ID NO:100) (CDRH2)  
GGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAXXXXXXXXXXXXXX  
(CDRH2 cont.)  
XXXAGAGTCACCATGAC  
(FRH3 - SEQ ID NO:101)  
CAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGA  
(CDRH3)  
GGACACGGCCGTGTATTACTGTGCGAGAXXXXXXXXXXXXXXXXXXXXXXXXXXX  
(CDRH3) (FRH4 - SEQ ID NO:102)  
XXXXXXXXXXXXXTGGGGCAAAGGGACCACGGTCACCGTCTCCTCA

## FIGURE 10

A.

**SEQ ID NO:67 - AME 33 complete light chain amino acid sequence**

EIVLTQSPGTL<sup>SL</sup>SPGERATL<sup>SCR</sup>ASSSVPIH<sup>WY</sup>QQKPGQAPRLLI<sup>YATS</sup>ALASGIPDR  
FSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLEIKRTVAAPS<sup>VFIFPPS</sup>  
DEQLKSGTASV<sup>VCLLN</sup>NFYPREAKVQWKVDNALQSGNSQESVTEQDSK<sup>DSTY</sup>SLST  
LTLSKADY<sup>EKH</sup>KVYACEVTHQGLSSPVTKSFNRGEC

- Constant Region is underlined

B.

**SEQ ID NO:68 - AME 33 complete light chain nucleic acid sequence**

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAG  
CCACCCTCTCCTGCAGGGCCAGCTCAAGTGTACCGTACATCCACTGGTACCAGCA  
GAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCCACATCCGCTCTGGCTTCTG  
GCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCAT  
CAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTGGCTGAGT  
AACCACCCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTG  
CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTACC  
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGGCCAAAGTACAGTGGA  
AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA  
CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA  
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG  
CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

## FIGURE 11

### A. SEQ ID NO:69 - AME 33 complete heavy chain amino acid sequence

EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTG  
DTSYNQKSKLQVTISADKSISTAYLQWSSLKASDTAMYYCARSTYVGGDWQFDVWG  
KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG  
VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH  
TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV  
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA  
KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV  
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

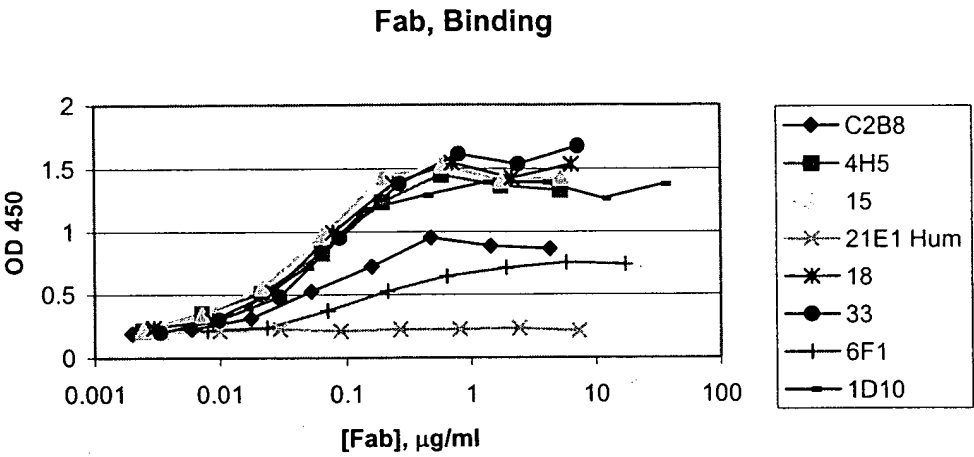
- Constant Region is underlined; the "D" at position 280 and "K" at position 290 are in bold

### B. SEQ ID NO:70 - AME 33 complete heavy chain nucleic acid sequence

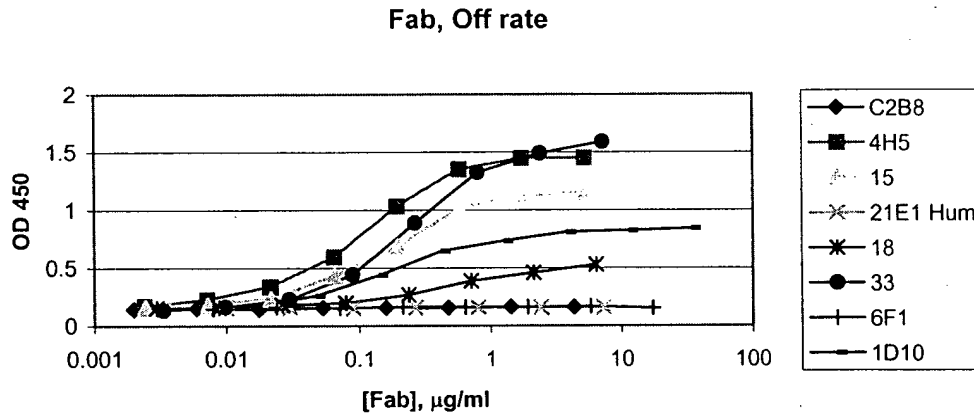
GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTG  
AAGATCTCCTGTAAGGGTTCTGGCCGTACATTTACCAGTTACAATATGCACTGGGT  
GCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGGCTATTTATCCCTTGACG  
GGTGATACTTCCTACAATCAGAAGTCGAAACTCCAGGTCACCATCTCAGCCGACA  
AGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGC  
CATGTATTACTGTGCGAGATCGACTTACGTGGGCGGTGACTGGCAGTTCGATGTCT  
GGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT  
CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT  
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGC  
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACT  
CCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT  
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTTGAGCC  
CAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG  
GGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTC  
CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG  
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG  
CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC  
TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG  
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGA  
ACCACAGGTGTACACCCTGCCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTC  
AGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGG  
AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC  
CGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA  
CGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

FIGURE 12

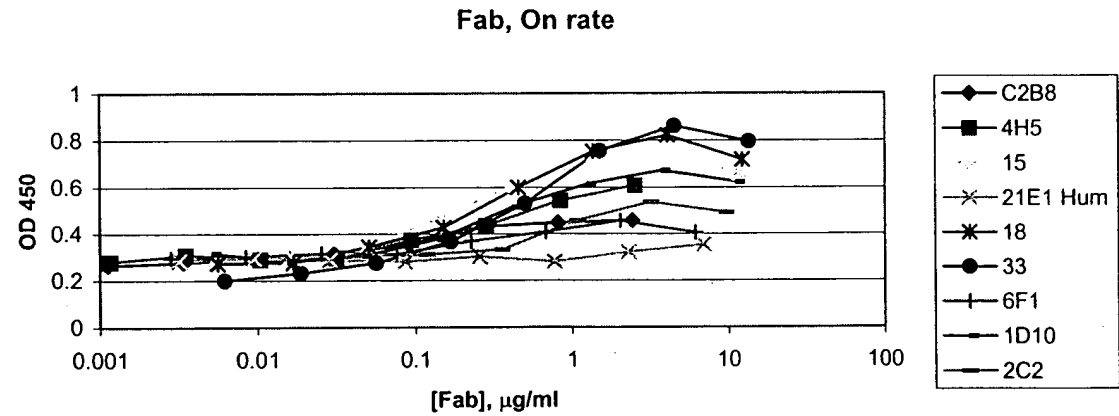
A.



B.



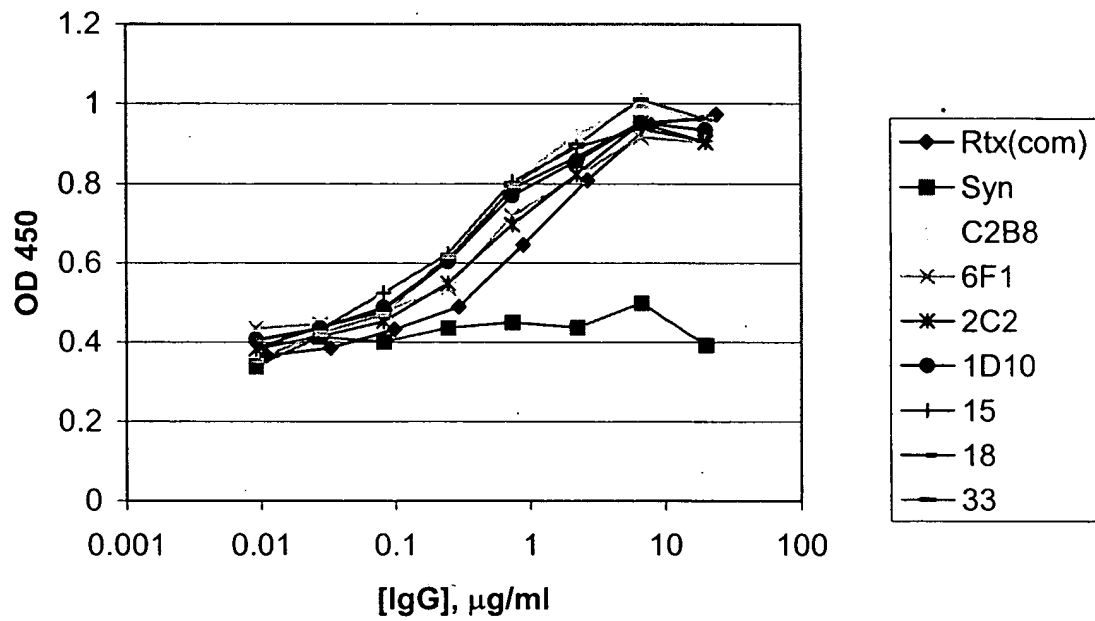
C.



A.

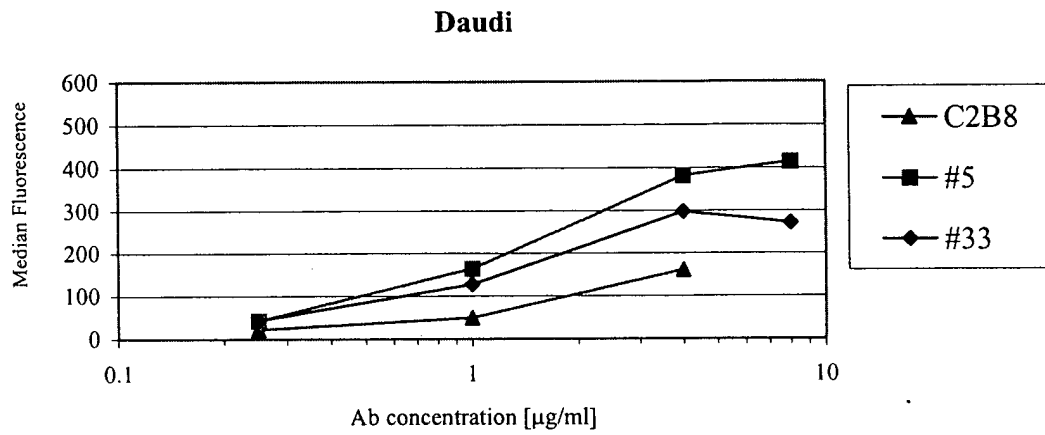
[illegible]

**IgG, On-rate**

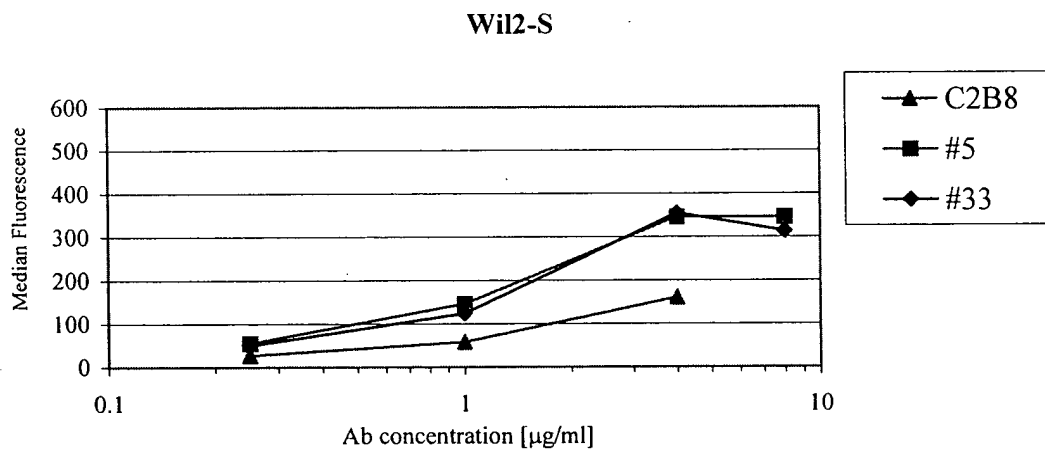


**FIGURE 14**

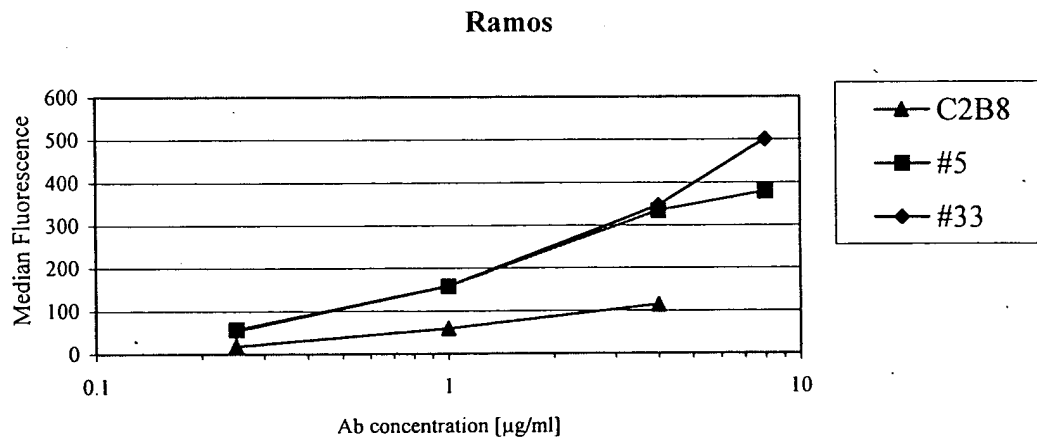
**A.**



**B.**



**C.**



**FIGURE 15**

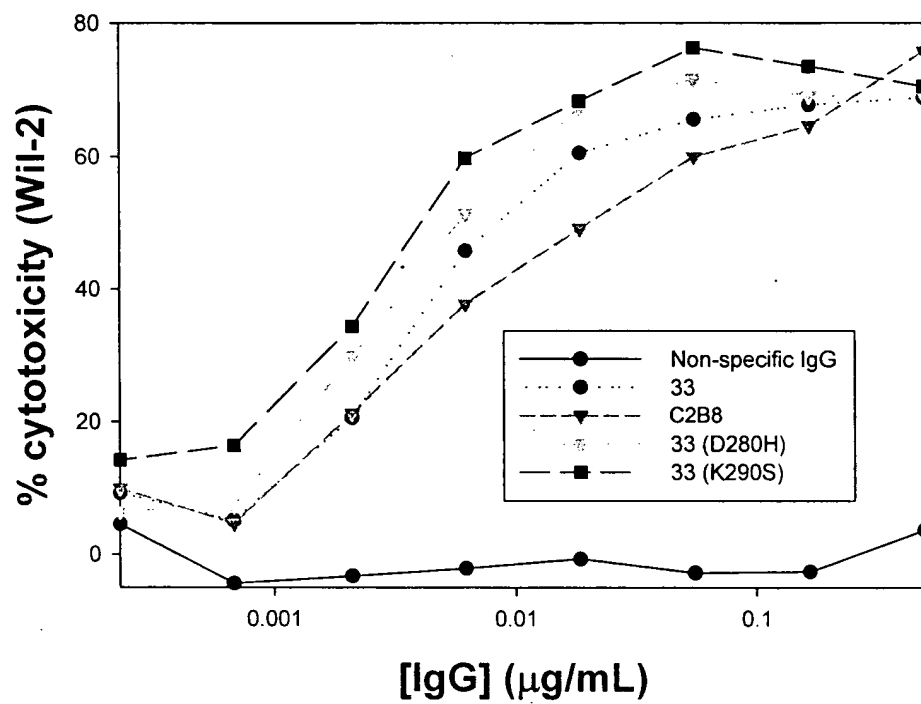
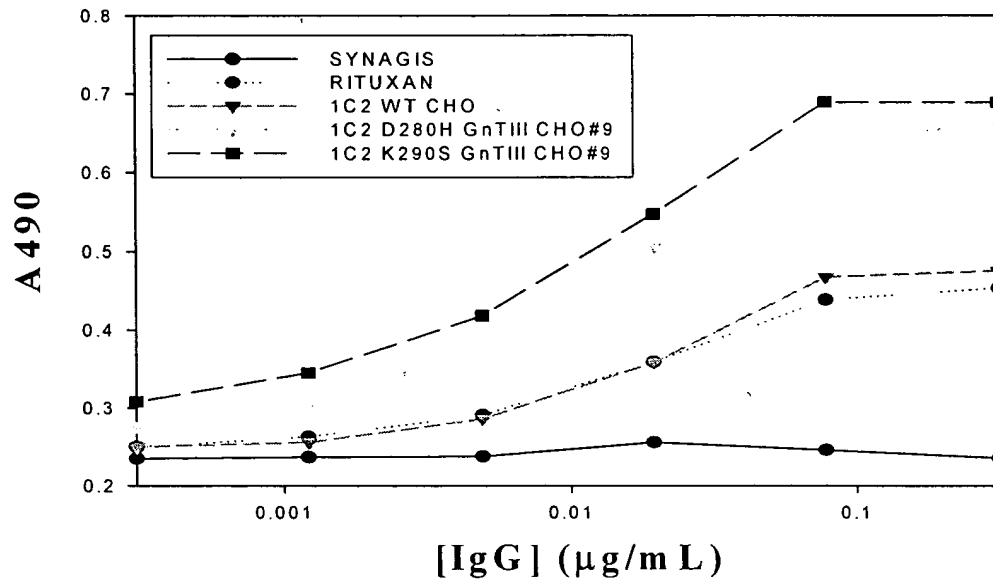
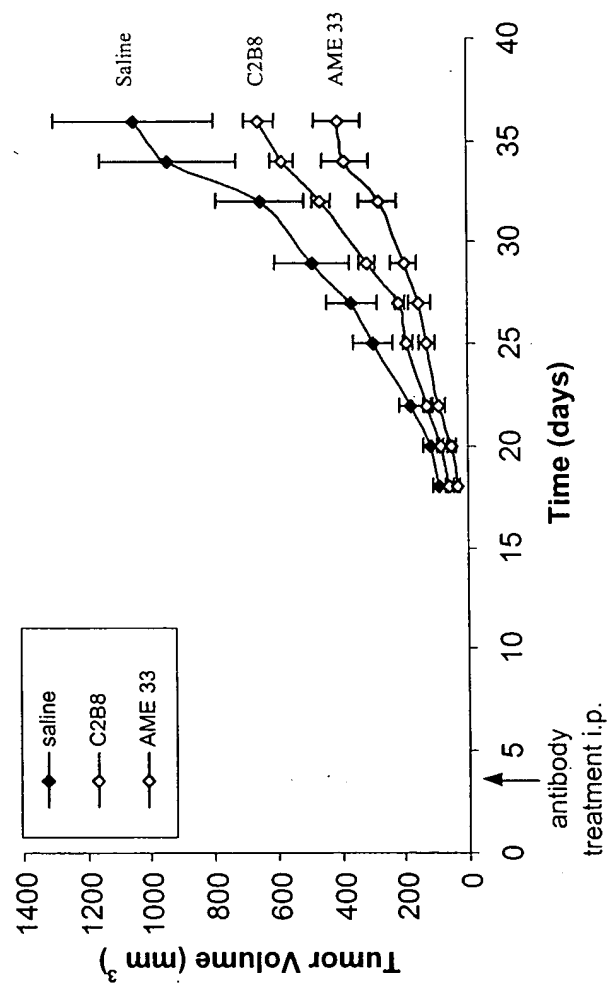


FIGURE 16







**FIGURE 17**